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RAW SEQUENCE LISTING

DATE: 04/09/2002

PATENT APPLICATION: US/10/088,045

TIME: 16:23:41

Input Set : N:\Crf3\04042002\J088045.raw

Output Set: N:\CRF3\04092002\J088045.raw

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1 <110> APPLICANT: Joelle Thonnard
2 <120> TITLE OF INVENTION: Novel Compounds
3 <130> FILE REFERENCE: BM45412
4 <140> CURRENT APPLICATION NUMBER: US/10/088,045
5 <141> CURRENT FILING DATE: 2002-03-14
6 <150> PRIOR APPLICATION NUMBER: 9921691.3
7 <151> PRIOR FILING DATE: 1999-09-14
8 <160> NUMBER OF SEQ ID NOS: 10
9 <170> SOFTWARE: FastSEQ for Windows Version 4.0
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1509
13 <212> TYPE: DNA
14 <213> ORGANISM: Moraxella catarrhalis
15 <400> SEQUENCE: 1
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17      agtggttgta gcaatcaagc ggacaaagcc gccagccaa aaagcagcac ggtagacgct      120
18      gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct      180
19      gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac      240
20      cccgccaag tggtggtaaa aatggaaacc gttgaaaaag tcatgcgtct gccagatggc      300
21      gtggaatata agttttggac atttggcggc caagttccag ggcagatgat tcgtgtgcgt      360
22      gaaggcgaca ccatcgaagt gcagttctca aaccacccag attcaaaaaat gccccataat      420
23      gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg      480
24      ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt      540
25      gcggttgccc ctgttgcat gcacattgct aatggcatgt atggtttgat tttggttgaa      600
26      caaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat      660
27      accaaaggca aatatggcga acaaggctca cagcccttg atatggaaaa agccattcga      720
28      gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct      780
29      ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg      840
30      acatcatcat tccatgtcat tggtagatt tttgataagg ttcaacttga ggttggttaag      900
31      ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa      960
32      ttttaagggtg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt      1020
33      aacaaagggg cattgggcat acttaagggt gaagggtgaag aaatcatga gatttattca      1080
34      cacaacaaa cagacgtgt ctatctgcca gaggtgccc cacaagcaat tgatacccaa      1140
35      gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggttaaggca      1200
36      acctagact ctaactgtgc tgcttgcac caacctgatg gtaaaggcgt gccaaacgct      1260
37      tccccaccgc ttgccaaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc      1320
38      gtggcaaatg gattgtcttg taagattacc gtcaatggca accaatatga aagcgtcatg      1380
39      cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc      1440
40      tttgtaaca aaggcggcga actcagtgcga gacgatgtgg caaaagccaa aaaaaccaag      1500
41      ccaaactga                                     1509
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 502
45 <212> TYPE: PRT

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46 <213> ORGANISM: Moraxella catarrhalis

47 <400> SEQUENCE: 2

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48 Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser
49 1 5 10 15
50 Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
51 20 25 30
52 Pro Lys Ser Ser Thr Val Asp Ala Ala Lys Thr Ala Asn Ala Asp
53 35 40 45
54 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
55 50 55 60
56 Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
57 65 70 75 80
58 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
59 85 90 95
60 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
61 100 105 110
62 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
63 115 120 125
64 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
65 130 135 140
66 Ala Ala Thr Gly Pro Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
67 145 150 155 160
68 Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
69 165 170 175
70 Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
71 180 185 190
72 Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
73 195 200 205
74 Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
75 210 215 220
76 Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
77 225 230 235 240
78 Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
79 245 250 255
80 Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
81 260 265 270
82 Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
83 275 280 285
84 Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
85 290 295 300
86 Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
87 305 310 315 320
88 Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
89 325 330 335
90 Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
91 340 345 350
92 Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
93 355 360 365
94 Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys

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95          370          375          380
96  Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
97  385          390          395          400
98  Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
99          405          410          415
100 Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
101          420          425          430
102 Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
103          435          440          445
104 Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
105          450          455          460
106 Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
107  465          470          475          480
108 Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
109          485          490          495
110 Lys Lys Thr Lys Pro Asn
111          500
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 1506
115 <212> TYPE: DNA
116 <213> ORGANISM: Moraxella catarrhalis
117 <400> SEQUENCE: 3
118 atgtctaagc ctactttgat aaaaacaacc ttaatttgtg ccttaagtgc attgatgctc 60
119 agtggttgta gcaatcaagc ggacaaagcc gccagccaa aaagcagcac ggtagacgct 120
120 gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct 180
121 gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac 240
122 cccgccaag tggtggtaaa aatggaaacc gttgaaaaag tcatgctgtc ggcagatggc 300
123 gtggaatatc agttttggac atttgcggt caagttccag ggcagatgat tcgtgtgcgt 360
124 gaaggcgaca ccatogaagt gcagttctca aaccacccag attcaaaaat gcccataat 420
125 gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg 480
126 ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt 540
127 gcggttgccc ctgttggcat gcacattgct aatggcatgt atggtttgat tttggttgaa 600
128 ccaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat 660
129 accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga 720
130 gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct 780
131 ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg 840
132 acatcatcat tccatgtcat tggtagatt tttgataagg ttcactttga ggttggttaag 900
133 ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa 960
134 ttttaaggtg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt 1020
135 aacaaagggg cattgggcat acttaaggtg gaaggtgaag aaaatcatga gatttattca 1080
136 cacaacaaa cagacgctgt ctatctgcca gaggtgccc cacaagcaat tgatacccaa 1140
137 gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggttaaggca 1200
138 acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct 1260
139 ttcccaccgc ttgccaaact tgactatctg aacgccgacc acgctcgtgc cgccagcatc 1320
140 gtggcaaatg gattgtcttg taagattacc gtcaatggca accaatatga aagcgtcatg 1380
141 cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc 1440
142 tttggttaaca aaggcgggtca actcagtgcg gacgatgtgg caaaagccaa aaaaaccaag 1500
143 ccaaac
144          1506
145 <210> SEQ ID NO: 4

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146 <211> LENGTH: 502
147 <212> TYPE: PRT
148 <213> ORGANISM: Moraxella catarrhalis
149 <400> SEQUENCE: 4
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153 20 25 30
154 Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
155 35 40 45
156 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
157 50 55 60
158 Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
159 65 70 75 80
160 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
161 85 90 95
162 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
163 100 105 110
164 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
165 115 120 125
166 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
167 130 135 140
168 Ala Ala Thr Gly Pro Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
169 145 150 155 160
170 Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
171 165 170 175
172 Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
173 180 185 190
174 Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
175 195 200 205
176 Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
177 210 215 220
178 Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
179 225 230 235 240
180 Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
181 245 250 255
182 Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
183 260 265 270
184 Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
185 275 280 285
186 Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
187 290 295 300
188 Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
189 305 310 315 320
190 Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
191 325 330 335
192 Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
193 340 345 350
194 Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr

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```

195          355          360          365
196  Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
197          370          375          380
198  Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
199  385          390          395          400
200  Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
201          405          410          415
202  Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
203          420          425          430
204  Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
205          435          440          445
206  Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
207          450          455          460
208  Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
209  465          470          475          480
210  Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
211          485          490          495
212  Lys Lys Thr Lys Pro Asn
213          500
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 21
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: primer
221 <400> SEQUENCE: 5
222  aagcgaacag ttctgccaac c
224 <210> SEQ ID NO: 6
225 <211> LENGTH: 23
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: primer
230 <400> SEQUENCE: 6
231  gggggcgcttg actggtgaaa atg
233 <210> SEQ ID NO: 7
234 <211> LENGTH: 17
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: primer
239 <400> SEQUENCE: 7
240  gtaaaacgac ggccagt
242 <210> SEQ ID NO: 8
243 <211> LENGTH: 17
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: primer

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,045

DATE: 04/09/2002

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Input Set : N:\Crf3\04042002\J088045.raw

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